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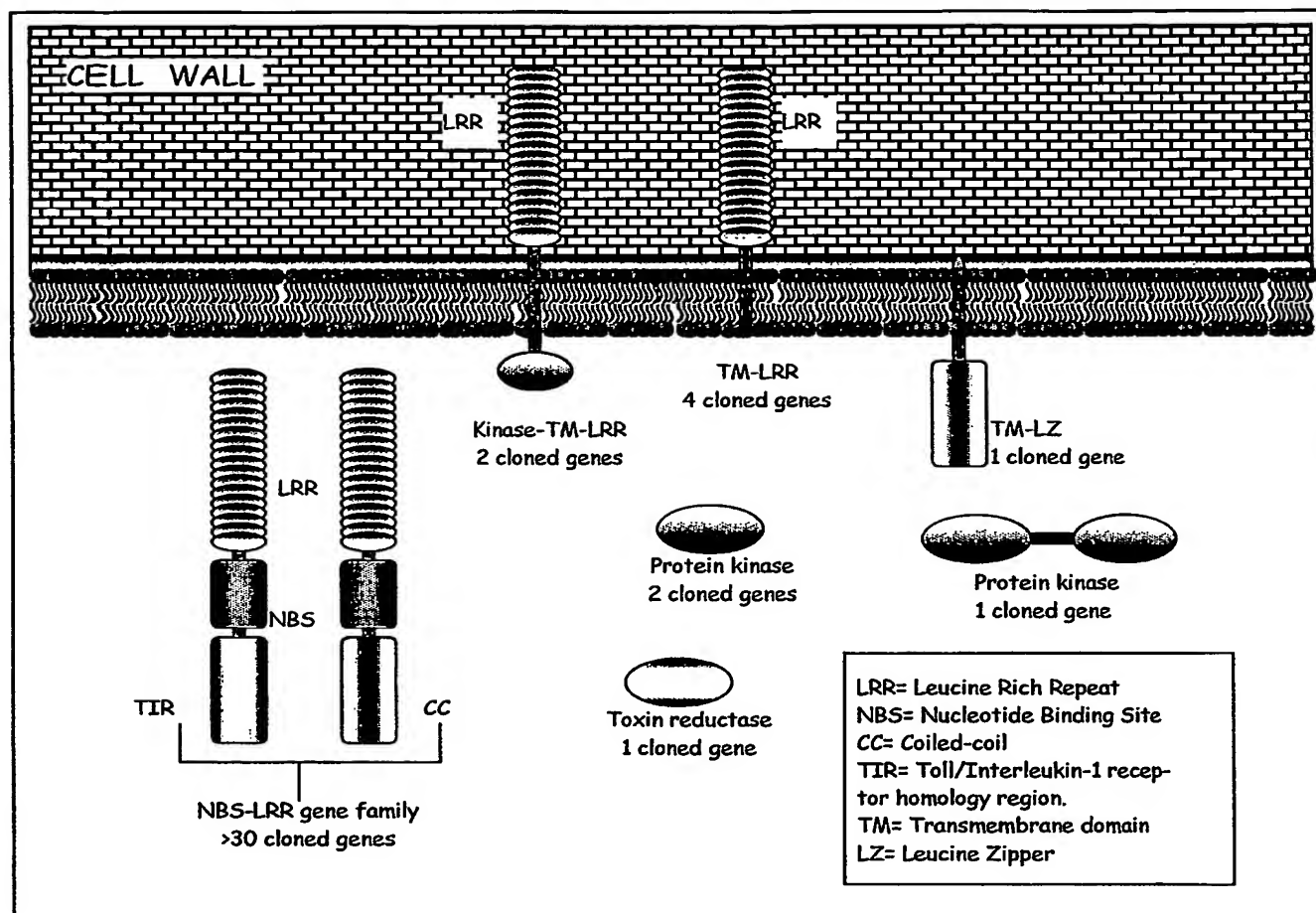


FIGURE 1

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		10	20	30	40	50	60	
RGA5	1	MS	TALVIGGWFAQSFIQTLLDKASNCATQOLARRRGLHDDLRRTSLLRIHAILDKAET	60				
RGA2	1	-MADVTPOAAAVFSLVNEIFNRSINLIVAEIRLOLNARAEINN	QRTLLRTHSLLEEAKA	59				
		70	80	90	100	110	120	
RGA5	61	RWNHKN	TSLVELVRQLKDAAYDAEELLEEYQAAKQVEHRGDQISDLFSFSLSTASEW	120				
RGA2	60	RR-MTDKSLVLWLMELKEWAYDADDILDEYFAAAIRLKVTR	---	S----	TFKRLIDHVI	110		
		130	140	150	160	170	180	
RGA5	121	LGADGDDAGTRLREIQGKLCNIAADMMDMVQLAPDDGGROFDWKVVRRETSSFLTETVV	180					
RGA2	111	INVP---	LAHKVADI	RKRLNGVTLERELNLGALE---	GSQPLDS-TKRGVITSLTSC	163		
		190	200	210	220	230	240	
RGA5	181	FGNDQEREKVVLELLDSGSGNSSFSVLPLVGI	GGVGGKTTLAQLVYNDNRVGNFYHLKVWV	240				
RGA2	164	VGRAQDKENLIRLLLEPSDG--	AVFVVPVIVGLGCAGKTTLSQLIFNDKRV	EEHFLRMWV	221			
		250	260	270	280	290	300	
RGA5	241	CVSDN	FNVKRLTKEIIESATKVEQSDKLNLDTLQQLKFKIASERFLLVLDVWSFN	NRDD	300			
RGA2	222	CVSDDE	EVKRLITREITEYATNGRFMLTNLNLQVNLKEEIRGTTFLVLVDVWNE	DPVK	281			
		310	320	330	340	350	360	
RGA5	301	WERLCAPLRF	AARGSKVIVTTRDTKIASITIGTMKEISLDGLDDAYWELEKKCAF	GSVN-	359			
RGA2	282	WESLLAPLDAGGRGS	VVIVTTQSKKVADVITGTMEPYVLEEITEDDSWSLIESHSFREASC	341				
		370	380	390	400	410	420	
RGA5	360	PQEHLE	LEVIGRKIAGNLKGSPLAAKTLGSLRLLDVSOEHWRPTIMESEVWOLPOAENEIL	419				
RGA2	342	SSTNPRMEE	IGRKIAKRTISGLPYGATAMGRYLRSKHGESSWREVLETETWEMPPAASDVL	401				
		430	440	450	460	470	480	
RGA5	420	PVLWLSYQHL	PGHIDROCFAFCAVFKHDYLFYKHETIQTWIAEGFTIAHQGNKRMEDVGSSY	479				
RGA2	402	SALRRSYDNL	PPOLKLCFAFCALFTKGYRFRKDTLIHMMWIAQNLIQSTESKRSEDMAECC	461				
		490	500	510	520	530	540	
RGA5	480	FHEI	VNRSFFQESRWRCRYVMHDLIHLLAQFISVGECHRIDDKSKETESTTRILSVALT	539				
RGA2	462	FDDI	VCRFFERYSGNVMNDSVHDLARWVSLDEYFRAEDSPLHISKPIRHLWCSE	519				
		550	560	570	580	590	600	
RGA5	540	EQMKLVDF	SGYN-KLRTLMINNQRNOYPYMTKVNSCLIPHSLEKRLKRIHVVLQKCGMK	598				
RGA2	520	RITNVLED	NNTGGDAVNPLSSLRTLFLGQSEFRSYHLLDRMFRMLSRIRVLDSENVIR	579				

FIGURE 2-1

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		610	620	630	640	650	660	
RGA5	599	ELPDITIGDLIQIRYLDISYNACTQRLPESLCDLYNLCATRLWGCOLRSEFQGM SKLINLR	658					
RGA2	580	NLPSSVGNLKHIRYLGLS-NTRIQRLPESVTRLCCLQTLLECELCRLPRSMSRI VKLR	638					
		670	680	690	700	710	720	
RGA5	659	QLRVEDEIISKIYEVGKLISLQELSAFKVLNNHGNKTAELSGITQLRSTLRITNLENVGS	718					
RGA2	639	QLKANPDVIADI AKVGRLIELQELKAYNVDDKKKGHTAELSAMNQLHGDLSIRNLQNV EK	698					
		730	740	750	760	770	780	
RGA5	719	KELASKAKLHRKQYIEALELEWAAGQVSSLEHPLLVS EEVILGLQPHHFLKSLTIRGYSG	778					
RGA2	699	TRESRKARLDEKOKIKLLDLRWADGRG---AGECDRDRKVLKGLRPHPNLRELSIKYYGG	755					
		790	800	810	820	830	840	
RGA5	779	ATVPSWLDVKKMLPNLGTILKLENCITRLEGLSYIGQLPHLKVLMKRMRVVKOMSHEL CGCT	838					
RGA2	756	TSSPSWMTDOYLPNMETIRLRSCARLTLEPCLGQLHILRHLHIDGMSOVROINLOFYGTG	815					
		850	860	870	880	890	900	
RGA5	839	KSKLFPRLFEELVLEDMPTLKKEEPNLAQLPCLKIHMKNMFAVKHIGRELYGDIESNCFLS	898					
RGA2	816	EVSGFPLELELINIRRMFSLEEWS-----EP	840					
		910	920	930	940	950	960	
RGA5	899	LEELVLQDMLTLEELPNLGQLPHLKVIMKNMSALKLIGRELCDSPREKIWFPRLEVLVLK	958					
RGA2	840	-----R-----RNCCYFPR-----	849					
		970	980	990	1000	1010	1020	
RGA5	959	NMLALEELPSLDNFRVSRFFASSVEVGHLFSATR NKWFPRL EELEIKGMLTFEELHSLE	1018					
RGA2	849	-----LH-----	851					
		1030	1040	1050	1060	1070	1080	
RGA5	1019	KLPCLKVFRIGKLPVKKIGHGLFDSTCQRECFPRLEDLVLS DMPAWEESWAEREELFS	1078					
RGA2	851	-----	851					
		1090	1100	1110	1120	1130	1140	
RGA5	1079	CLCRIKIEQCPKIKCLLPPIPHSLIKLELWQVGLTG LPGLCKGIGGGSSTRTASLSLLHTI	1138					
RGA2	851	---KLLIEDCPRLRNLP SLPTLEELRTISRTGLVDLPG-FH---ENG DVTNVSLSLSLHVS	905					
		1150	1160	1170	1180	1190	1200	
RGA5	1139	KCPNLRNIGEGLLSNHTPHINAIRIWECAELLWLFPVKRFREFTTLENLSIRNCPKLM SMT	1198					
RGA2	906	ECRELRSLSEGLLOHNVALKTA AFTDCDSLEFLPAEGFRTAISLESIMTNCP--LP CS	963					

FIGURE 2-2

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		1210	1220	1230	1240	1250	1260	
RGA5	1199	QCEENDLLLPPLIKALELGDG	---	NLGKSLPGCLHNLS	SLTOLATSNCPYMVSLPREVM			1255
RGA2	963	-----FLIIPSSLEHLKIQPCLYPNNEDSI	STCFENLTSLSFIDIKDCPNLSSEFP	PGPI				1017
		1270	1280	1290	1300	1310	1320	
RGA5	1256	LHLKELGTVRIENC	DGLGSL	EGLVKSLKRLAIGCPRLILNE	-----	GDEQGEVLS		1308
RGA2	1018	COLSALOHLISLVN	CORLOSIG	-EQALTSLES	LTIONCPRLTMSHSLVEVNNS	SDTGLAFN		1076
		1330	1340	1350	1360	1370	1380	
RGA5	1309	LLELSVDKT	---	ALLKLSLTKN	---	TLPFIHSLRIIWS	PQKVMFDLEE	QELVHS 1356
RGA2	1077	ITRWRRRT	GDGGLMLRHRAQ	NDSSF	GGLLOHLTFLOFLKICQCPQ	LVTFTEGEE	EKKWRN	1136
		1390	1400	1410	1420	1430	1440	
RGA5	1357	ITAIRRTIEFFRCKN	QSLPTELHTLPSLHAI	VVSDCPQIQSLPEKGLPTLLTDI	GFDHCH			1416
RGA2	1137	ITSTQIIHIVDCPN	LEVLPANLOSLCSI	STIYIVRCPRIHAF	PPGGVSM	SLAHIVTHECP		1196
		1450	1460	1470				
RGA5	1417	PVLT	-----	AQLEKHLAEMK	---	SSGRFHPVYA	---	1441
RGA2	1197	QICQRC	PPGGDDWPLIANVPRIC	LGRTHPCRCSTT				1232

FIGURE 2-3

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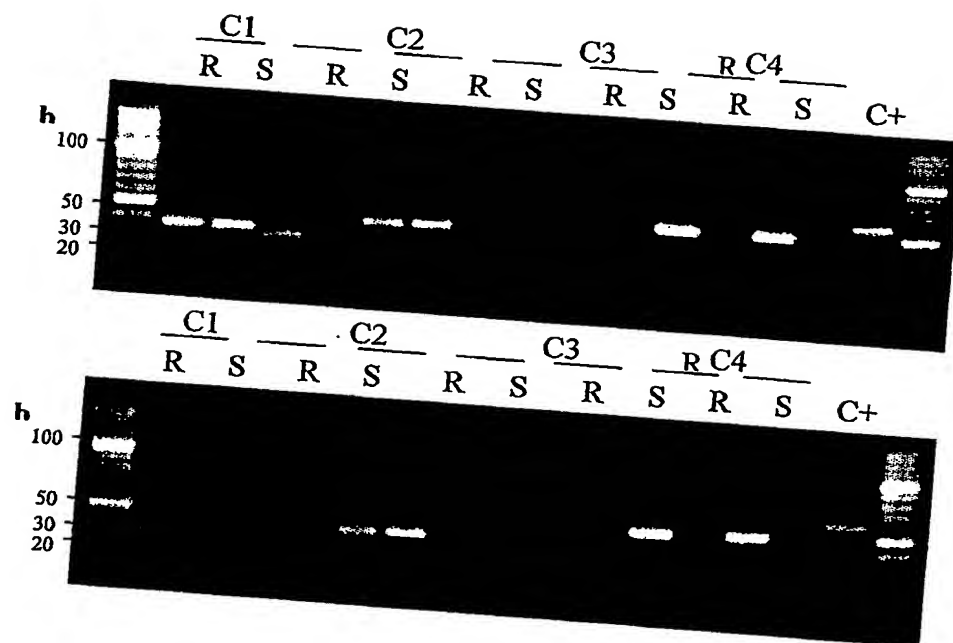


FIGURE 3